



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 116491

**TO:** Jeffrey Parkin  
**Location:** REM-3D39/3C18  
**Art Unit:** 1648  
**Monday, March 15, 2004**  
**Case Serial Number:** 10/055524

**From:** Paul Schulwitz  
**Location:** Biotech-Chem Library  
**REM-1A65**  
**Phone:** (571)272-2527  
  
**paul.schulwitz@uspto.gov**

### Search Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2527

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GanCore version 5.1.6  
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On protein - protein search, using sw model  
Run on: March 12, 2004, 14:22:45 ; Search time 54 Seconds  
(w/o alignments)  
52.324 Million cell updates/sec

Title: PARKIN524.PEP  
Perfect score: 46  
Sequence: 1 kpvvstqlll 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Genesed 29Jan04;\*

1: geneseqP1980s;\*  
2: geneseqP1990s;\*  
3: geneseqP2000s;\*  
4: geneseqP2001s;\*  
5: geneseqP2002s;\*  
6: geneseqP2003as;\*  
7: geneseqP2003bs;\*  
8: geneseqP2004as;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	46	100.0	10 4	ABP16652; abp16652 HIV B07 s
2	46	100.0	10 6	Abu69833 Human imm
3	46	100.0	10 6	Abu70212 Human imm
4	46	100.0	10 6	Abu70010 Human imm
5	46	100.0	10 7	Add96745 HIV-1 cro
6	46	100.0	10 7	Add96543 HIV-1 cro
7	46	100.0	10 7	Add96426 HIV-1 cro
8	46	100.0	11 4	Abp170799 HIV B27 s
9	46	100.0	15 4	Abp24380 HIV DR su
10	46	100.0	15 4	Abp24379 HIV DR su
11	46	100.0	15 4	Abp24416 HIV DR su
12	46	100.0	229 5	Abm48947 HIV-1 sub
13	46	100.0	236 5	hae15742 Plasmid C
14	46	100.0	417 2	Aaw43071 HIV-1 gp1
15	46	100.0	417 2	Aaw37067 HIV-1 bre
16	46	100.0	474 2	Aaw37066 HIV-1 bre
17	46	100.0	478 7	Aab39557 HIV gp120
18	46	100.0	478 7	Aab39558 HIV gp120
19	46	100.0	498 2	Aaw37055 HIV-1 bre
20	46	100.0	498 2	Aaw37054 HIV-1 bre
21	46	100.0	501 7	Aae39544 HIV gp120
22	46	100.0	501 7	Aae39543 HIV gp120
23	46	100.0	586 2	Aar49855 Sequence
24	46	100.0	587 2	Aay29900 Human MCP
25	100.0	591 2	Aar49856 Sequence	

ALIGNMENTS

RESULT 1	ABP16652	standard; peptide; 10 AA.
ID	ABP16652;	
XX	ABP16652;	
XX		
XX		
DT	11-SEP-2003	(revised)
DT	15-JUL-2002	(first entry)
XX		
DE	HIV B07 super motif env peptide #32.	
XX		
KW	HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.	
XX		
OS	Human immunodeficiency virus 1.	
XX		
PN	WO200124810-A1.	
XX		
PD	12-APR-2001.	
XX		
PP	05-OCT-2000; 99US-00412863.	
XX		
(EPBM-) EPIMMUNE INC.		
XX		
PI	Sette A, Sidney J, Southwood S, Livingston BD, Cheasnut R; Baker DM, Celis E, Kubo RT, Grey HM;	
PI		
XX		
DR	WPI; 2001-354887/37.	
XX		
Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.		
PT		
XX		
PS	Claim 32; Page 209; 448pp; English.	
XX		
The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABL25397). (I) has virucide activity and can be used in vaccines. (II) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or		

tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (C1L and H1L), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. AB11501 to AB25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.  
 CC (Updated on 23-OCT-2003 to standardise OS field)  
 XX  
 SQ sequence 10 AA:  
 Query Match Best Local Similarity Score 46; DB 6; Length 10;  
 Matchers 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KPVVSTQQLL 10  
 DB 1 KPVVSTQQLL 10

Qy	Db	Query Match Best Local Similarity Matches	Score 46; DB 4; Length 10; 0.0%; Pred. No. 0.01; 0; 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 2 ABU69893 ID ABU69893 standard; peptide; 10 AA. XX AC ABU69893; XX DT 23-OCT-2003 (revised) DT 05-JUN-2003 (first entry) XX DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #211. XX KW Human immunodeficiency virus; HIV; vaccine; immunological excipient; KW anti-HIV immune response; T cell response; KW viral multiplication inhibitor; chronic viraemia; AIDS. XX OS Human immunodeficiency virus 1. XX PN US2002182222-A1. XX XX PD 05-DEC-2002. XX PF 26-OCT-2001; 2001US-00055524. XX PR 10-JUL-1998; 98US-0092346P. PR 08-JAN-1999; 99US-0115145P. PR 23-APR-1999; 99US-013057P. PR 09-JUL-1999; 99US-00351036. XX PA (GROO/) GROOT A D. XX PI Groot AD; XX DR WPI; 2003-352642/33. XX PT New vaccine comprising human immunodeficiency virus (HIV) vaccine PT candidate peptides, useful as antigens for raising anti-HIV immune PT responses, such as T cell responses, and for inducing antibodies and PT impairing viral multiplication. XX PS Claim 1; Page 19; 32pp; English. XX CC The invention describes a vaccine comprising a human immunodeficiency CC virus (HIV) vaccine candidate peptide containing an amino acid sequence CC selected from 669 amino acid sequences given in the specification, in an CC immunological excipient. The HIV vaccine peptides are useful as antigens CC for raising anti-HIV immune responses, such as T cell responses, and for CC inducing antibodies that react with HIV-1 and impairing viral CC multiplication in vivo. These antibodies reduce viral multiplication CC during any initial acute infection with HIV-1 and minimise chronic CC viraemia or progression leading to AIDS. This is the amino acid sequence CC (Updated on 23-OCT-2003 to standardise OS field) XX SQ Sequence 10 AA; Query Match 100.0%; Score 46; DB 6; Length 10; Best Local Similarity 100.0%; Pred. No. 0.01; 0; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
				RESULT 3 ABU70212 ID ABU70212 standard; peptide; 10 AA. XX AC ABU70212; XX DT 23-OCT-2003 (revised) DT 05-JUN-2003 (first entry) XX DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #530. XX KW Human immunodeficiency virus; HIV; vaccine; immunological excipient; KW anti-HIV immune response; T cell response; KW viral multiplication inhibitor; chronic viraemia; AIDS.

QY	1	KPVNSTQLL 10	AC	ADD36745;
Db	1	KPVNSTQLL 10	XX	29-JAN-2004 (first entry)
XX			DE	HIV-1 cross-clade candidate peptide #530.
XX			XX	HIV-1; cross-clade candidate peptide; HIV clade;
ABU0010			XX	KW major histocompatibility complex; MHC; human leukocyte antigen; HLA;
ID			XX	T-cell activation; HIV positive patient; HIV infection; anti-HIV.
AC			OS	Human immunodeficiency virus 1.
XX			XX	US2003180314-A1.
DT	05-JUN-2003	(revised)	PN	US2003180314-A1.
DT	05-JUN-2003	(first entry)	XX	
DE	Human immunodeficiency virus 1 (HIV) vaccine candidate peptide #328.	XX		
XX			PD	25-SEP-2003.
KW	Human immunodeficiency virus; HIV; vaccine; immunological excipient;	XX	PP	22-JUL-2002; 2002US-0020070B.
KW	anti-HIV immune response; T cell response; chronic viraemia; AIDS.	XX	PR	10-JUL-1998; 98US-0092346P.
KW	viral multiplication inhibitor; chronic viraemia; AIDS.	PR	08-JAN-1999; 99US-0115145P.	
OS	Human immunodeficiency virus 1.	PR	23-APR-1999; 99US-0130677P.	
XX	US2002182222-A1.	PR	09-JUL-1999; 99US-00351036.	
PN		PA	(DEGR/) DEGROOT A.	
XX		XX		
PD	05-DEC-2002.	PT		
XX		XX		
PF	26-OCT-2001; 2001US-00055524.	PT		
XX		XX		
PR	10-JUL-1998; 98US-0092346P.	PT		
PR	08-JAN-1999; 99US-0115145P.	PT		
PR	23-APR-1999; 99US-0130677P.	PT		
PR	09-JUL-1999; 99US-00351036.	PT		
XX		XX		
PA	(GROO/) GROOT A. D.	PS		
XX		XX		
PI	Groot AD;	XX		
XX		PT	Degroot A;	
DR	WPI; 2003-3526642/33.	XX		
XX		DR	WPI; 2003-852210/79.	
PT	New vaccine comprising human immunodeficiency virus (HIV) vaccine	XX		
PT	candidate peptides, useful as antigens for raising anti-HIV immune	PT		
PT	responses, such as T cell responses, and for inducing antibodies and	PT		
PT	impairing viral multiplication.	PT		
XX		XX		
PS	Claim 1; Page 16; 32pp; English.	XX		
XX		CC	The present invention relates to HIV-1 cross-clade candidate peptides	
CC		CC	comprising a sequence of about 8-50 amino acids, the sequence having	
CC		CC	complete, sequential sequence identity with a partial HIV-1 amino acid	
CC		CC	sequence that is absolutely conserved across at least 2 clades of HIV.	
CC		CC	The HIV-1 cross-clade candidate peptides possess at least one of the	
CC		CC	biological properties selected from (i) the ability to bind a human major	
CC		CC	histocompatibility complex (MHC) binding matrix motif for a human MHC	
CC		CC	allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the	
CC		CC	T2 in vitro peptide binding assay, and (iii) the ability to activate T-	
CC		CC	cells from HIV positive patients in at least one in vitro assay. The	
CC		CC	invention also discloses a pharmaceutical composition comprising the	
CC		CC	above peptide, and methods for the production and use of the cross-clade	
CC		CC	peptides. The composition and methods are useful in preventing or	
CC		CC	treating HIV infection. The present sequence represents a HIV-1 cross-	
CC		CC	clade candidate peptide.	
SQ	Sequence 10 AA;	XX		
Query Match	100.0%; Score 46; DB 6; Length 10;	XX		
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 KPVNSTQLL 10	XX		
Db	1 KPVNSTQLL 10	XX		
RESULT 5		XX		
ID	ADD36745 standard; peptide; 10 AA.	XX		
XX		XX		
Query Match	100.0%; Score 46; DB 7; Length 10;	XX		
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 KPVNSTQLL 10	XX		
Db	1 KPVNSTQLL 10	XX		
RESULT 6		XX		
ID	ADD36543 standard; Peptide; 10 AA.	XX		
XX		XX		
AC	ADD36543;	XX		
XX		XX		
DT	29-JAN-2004 (first entry)	XX		
XX		DE		
DE	HIV-1 cross-clade candidate peptide #328.	XX		
XX		HIV-1; cross-clade candidate peptide; HIV clade;		

KW major histocompatibility complex; MHC; human leukocyte antigen; HLA;  
 XX T-cell activation; HIV positive patient; HIV infection; anti-HIV.  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2003180314-A1.  
 XX  
 PD 25-SEP-2003.  
 XX  
 PF 22-JUL-2002; 2002US-00200708.  
 XX  
 PR 10-JUL-1998; 98US-00923346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.  
 XX  
 PA (DEGR/) DEGROOT A.  
 XX  
 PI Degroot A;  
 XX  
 DR WPI; 2003-852210/79.  
 XX  
 PT New cross-clade HIV candidate peptide that binds a human major  
 PT histocompatibility complex binding matrix motif or activates T-cells from  
 PT HIV positive patients, useful for preventing or treating HIV infection.  
 PS Example 3; SEQ ID NO 328; 146pp; English.  
 XX  
 CC The present invention relates to HIV-1 cross-clade candidate peptides  
 CC comprising a sequence of about 8-50 amino acids, the sequence having  
 CC complete, sequential sequence identity with a partial HIV-1 amino acid  
 sequence that is absolutely conserved across at least 2 clades of HIV.  
 CC The HIV-1 cross-clade candidate peptides possess at least one of the  
 CC biological properties selected from (i) the ability to bind a human major  
 CC histocompatibility complex (MHC) binding matrix motif for a human MHC  
 CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the  
 CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-  
 CC cell from HIV positive patients in at least one in vitro assay. The  
 CC invention also discloses a pharmaceutical composition comprising the  
 CC above peptide, and methods for the production and use of the cross-clade  
 CC peptides. The composition and methods are useful in preventing or  
 CC treating HIV infection. The present sequence represents a HIV-1 cross-  
 CC clade candidate peptide.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 46; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KPVNSTQLL 10  
 Db 1 KPVNSTQLL 10  
 XX  
 RESULT 7  
 ADD96425  
 ID ADD96426 standard; Peptide; 10 AA.  
 XX  
 AC ADD96426;  
 XX  
 DT 29-JAN-2004 (first entry)  
 DE HIV-1 cross-clade candidate peptide #211.  
 XX  
 KW HIV-1; cross-clade candidate peptide; HIV clade;  
 KW major histocompatibility complex; MHC; human leukocyte antigen; HLA;  
 KW T-cell activation; HIV positive patient; HIV infection; anti-HIV.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2003180314-A1.

PD 25-SEP-2003.  
 XX  
 PF 22-JUL-2002; 2002US-00200708.  
 XX  
 PR 10-JUL-1998; 98US-00923346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.  
 XX  
 PA (DEGR/) DEGROOT A.  
 XX  
 PI Degroot A;  
 XX  
 DR WPI; 2003-852210/79.  
 XX  
 PT New cross-clade HIV candidate peptide that binds a human major  
 PT histocompatibility complex binding matrix motif or activates T-cells from  
 PT HIV positive patients, useful for preventing or treating HIV infection.  
 PS Example 3; SEQ ID NO 211; 146pp; English.  
 XX  
 CC The present invention relates to HIV-1 cross-clade candidate peptides  
 CC comprising a sequence of about 8-50 amino acids, the sequence having  
 CC complete, sequential sequence identity with a partial HIV-1 amino acid  
 sequence that is absolutely conserved across at least 2 clades of HIV.  
 CC The HIV-1 cross-clade candidate peptides possess at least one of the  
 CC biological properties selected from (i) the ability to bind a human major  
 CC histocompatibility complex (MHC) binding matrix motif for a human MHC  
 CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the  
 CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-  
 CC cell from HIV positive patients in at least one in vitro assay. The  
 CC invention also discloses a pharmaceutical composition comprising the  
 CC above peptide, and methods for the production and use of the cross-clade  
 CC peptides. The composition and methods are useful in preventing or  
 CC treating HIV infection. The present sequence represents a HIV-1 cross-  
 CC clade candidate peptide.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 46; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KPVNSTQLL 10  
 Db 1 KPVNSTQLL 10  
 XX  
 RESULT 8  
 ABP17099  
 ID ABP17099 standard; peptide; 11 AA.  
 XX  
 AC ABP17099;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)  
 DE HIV B27 super motif env peptide #124.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunization; virucide.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX

PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 219; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to  
 ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 11 AA;

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%	46	4	11		
Qy 1 KPVVSTIQLLL 10						
Db 2 KPVVSTIQLLL 11						

RESULT 9

ID	ABP24380	ABP24380 standard; peptide; 15 AA.
AC	ABP24380;	
XX		
DT	11-SEP-2003 (revised)	
DT	15-JUL-2002 (first entry)	
XX	HIV DR super motif env peptide #2.	
DE	HIV DR super motif env peptide #2.	
XX	HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.	
XX	OS Human immunodeficiency virus 1.	
OS	Human immunodeficiency virus 1.	
PN	WO200124810-A1.	
XX		
PD	12-APR-2001.	
XX		
PP	05-OCT-2000; 2000WO-US027766.	
PR	05-OCT-1999; 99US-00412863.	
XX		
XX	(EPIM-) EPIMMUNE INC.	
XX		
PA	Baker DM, Celis E, Kubo RT, Grey HM;	
PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;	

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 369; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to  
 ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 15 AA;

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%	46	4	15		
Qy 1 KPVVSTIQLLL 10						
Db 2 KPVVSTIQLLL 11						

RESULT 10

ID	ABP24379	ABP24379 standard; peptide; 15 AA.
AC	ABP24379;	
XX		
DT	11-SEP-2003 (revised)	
DT	15-JUL-2002 (first entry)	
XX	HIV DR super motif env peptide #1.	
XX	HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.	
XX	OS Human immunodeficiency virus 1.	
PN	WO200124810-A1.	
XX		
PD	12-APR-2001.	
XX		
PP	05-OCT-2000; 2000WO-US027766.	
PR	05-OCT-1999; 99US-00412863.	
XX		
XX	(EPIM-) EPIMMUNE INC.	
XX		
PA	Baker DM, Celis E, Kubo RT, Grey HM;	
PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;	



PT Selecting HIV-1 subtype C isolates, which are useful in developing  
PT vaccines against HIV infection, comprises isolating viruses with high  
PT sequence identity to a consensus sequence whose phenotype is associated  
PT with the HIV subtype.

PS Claim 26; Page 37; 63pp; English.

XX

CC The present invention relates to a process for the selection of human  
CC immunodeficiency virus (HIV) subtype isolates for use in the development  
CC of a prophylactic and/or therapeutic pharmaceutical composition. The  
process involves selecting isolated virus or viruses with a high sequenc  
CC identity to a consensus sequence and a phenotype which is associated with  
CC transmission for the particular HIV subtype. The composition can be used  
CC in the production of vaccines against HIV. The present sequence is a  
CC consensus sequence for the HIV-1 subtype C env protein. (Updated on 29-  
CC AUG-2003 to standardise OS field)

SQ Sequence 229 AA:

XX

FT Misc-difference 147  
FT /note= "Encoded by TTT"  
FT Misc-difference 163  
FT /note= "Encoded by CCA"  
FT Misc-difference 223  
FT /note= "Encoded by AAA"  
XX PN WO200176643-A1.  
XX PR 06-APR-2001; 2001WO-US011372.  
XX PR 07-APR-2000; 2000US-0195680P.  
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PI Orson FM, Kinsey BM, Bhogal BS;

Query	Match	Score	DB	Length
QY	KPVVSTQLL	10	5	229
Db	KPVVSTQULL	45		

Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0.

DR  
WPI; 2002-063308/09.  
N-FSDB; AAD25513.

XX

PT Composition for oral delivery of vaccines, comprises expression vector  
PT containing antigenic genomic sequence, bound to aggregated protein-  
PT polycationic polymer conjugate or suspension.

XX

TRADE NO. 10 REG. NO. 76 14520. POLISH

**RESULT 13**

AAE15742	CC	The invention relates to a composition comprising an expression vector
XX	CC	bound to an aggregated protein-polycationic polymer conjugate or
ID AAE15742 standard; protein; 236 AA.	CC	suspension. The expression vector contains a promoter polynucleotide
XX	CC	sequence operatively linked to a polynucleotide sequence encoding an
AC AAE15742;	CC	antigen which is a fragment of a gene or genome associated with an
XX	CC	infectious disease, cancer and autoimmune disease such as rheumatoid
DT 29-AUG-2003 (revised)	CC	arthritis, vasculitis, and multiple sclerosis; pathogenic genomes
DT 26-MAR-2002 (first entry)	CC	consisting of bacterium, fungi, protozoa and virus such as human
XX	CC	immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C
DE Plasmid CMV-HIV UB-#23 DNA encoded protein.	CC	virus (HCV), influenza and respiratory syncytial virus (RSV), and
XX	CC	optionally comprising a nucleotide sequence encoding a cytokine (or a
KW HIV; human immunodeficiency virus; CMV; cytomegalovirus; cytostatic;	CC	cytokine expression vector), is useful for inducing an immune response
KW immunosuppressive; viricide; antibacterial; fungicide; protozoicide;	CC	(systemic and/or mucosal) in an organism. The cytokine expression vector
KW antirheumatic; antiinflammatory; antiarthritic; neuroprotective;	CC	contains a sequence for granulocyte macrophage-colony stimulating factor
KW rheumatoid arthritis; cancer; multiple sclerosis; immune response;	CC	(GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding
KW vasoconstrictor; vaccine; gene therapy; autoimmune disease; vasculitis;	CC	the antigen and the cytokine are under transcriptional control of same or
KW ubiquitin.	CC	different promoter polynucleotide sequences. The expression vector, as a
XX DNA vaccine is useful for treating a condition in an organism. The	CC	present sequence is protein encoded by plasmid CMV-HIV UB-#23 DNA. The
OS protein contains ubiquitin fused to a protein fragment containing the	CC	immunodominant epitope for gp120, related to the invention. (Updated on
OS ChimERIC.	CC	26-MAR-2002 to standardize OS field)





QY 1 KPVVSTQILL 10 ; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
Db 207 KPVVSTQILL 216 ; FILE REFERENCE: 14918-703C1P  
; CURRENT APPLICATION NUMBER: US/09419362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841B  
; PATENT NO. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703D1V1  
; CURRENT APPLICATION NUMBER: US/09/419,362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: HIV  
US-09-419-362-36 ; US-08-889,841B-2  
Query Match 100.0%; Score 46; DB 4; Length 474;  
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; ;  
QY 1 KPVVSTQILL 10 ; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
Db 207 KPVVSTQILL 216 ; FILE REFERENCE: 14918-703C1P  
; CURRENT APPLICATION NUMBER: US/08/889,841B  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: HIV  
US-09-419-362-39 ; US-08-889-841B-5  
Query Match 100.0%; Score 46; DB 3; Length 498;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; ;  
QY 1 KPVVSTQILL 10 ; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
Db 232 KPVVSTQILL 241 ; FILE REFERENCE: 14918-703C1P  
; CURRENT APPLICATION NUMBER: US/08/889,841B  
; CURRENT FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: HIV  
US-09-419-362-39 ; US-08-889-841B-5  
Query Match 100.0%; Score 46; DB 4; Length 474;  
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; ;  
QY 1 KPVVSTQILL 10 ; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
Db 232 KPVVSTQILL 241 ; FILE REFERENCE: 14918-703C1P  
; CURRENT APPLICATION NUMBER: US/09419362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US/09/419,362  
; PATENT NO. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVIRONMENTAL POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703D1V1  
; CURRENT APPLICATION NUMBER: US/08/889,841  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 39  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: HIV  
US-09-419-362-39 ; US-08-889-841B-5  
Query Match 100.0%; Score 46; DB 3; Length 498;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; ;  
QY 1 KPVVSTQILL 10 ; TITLE OF INVENTION: HIV ENVIRONMENTAL POLYPEPTIDES AND VACCINE  
Db 232 KPVVSTQILL 241 ; FILE REFERENCE: 14918-703D1V1  
; CURRENT APPLICATION NUMBER: US/09419362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US/09/419,362  
; PATENT NO. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVIRONMENTAL POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703D1V1  
; CURRENT APPLICATION NUMBER: US/09/419,362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 498

;

; TYPE: PRT

; ORGANISM: HIV

; US-09-419-362-2

Query Match Best Local Similarity 100.0%; Score 46; DB 4; Length 498; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 .KPVVSTQLL 10

Db 232 KPVVSTQLL 241

RESULT 8

US-09-362-5

; Sequence 5, Application US/09419362

; Patent No. 6585979

; GENERAL INFORMATION:

; APPLICANT: Berman, Phillip W.

; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE

FILE REFERENCE: 14918-703D1V1

CURRENT APPLICATION NUMBER: US/09/419,362

CURRENT FILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: US 08/889,841

PRIOR FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: US 60/676,737

PRIOR FILING DATE: 1996-07-08

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 498

TYPE: PRT

ORGANISM: HIV

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)..(498)

; OTHER INFORMATION: xaa = Any Amino Acid

US-09-419-362-5

Query Match Best Local Similarity 100.0%; Score 46; DB 4; Length 498; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10

Db 232 KPVVSTQLL 241

RESULT 9

US-09-646-028-50

; Sequence 50, Application US/09646028

; Patent No. 6562347

; GENERAL INFORMATION:

; APPLICANT: Kwak, Larry

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: US/08/392,806A

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 50

LENGTH: 587

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-56

Query Match Best Local Similarity 100.0%; Score 46; DB 4; Length 595; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10

Db 336 KPVVSTQLL 345

RESULT 10

US-09-646-028-56

; Sequence 56, Application US/09646028

; Patent No. 6562347

; GENERAL INFORMATION:

; APPLICANT: Kwak, Larry

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 56

LENGTH: 595

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-56

Query Match Best Local Similarity 100.0%; Score 46; DB 4; Length 595; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10

Db 336 KPVVSTQLL 345

RESULT 11

US-09-392-806A-2

; Sequence 2, Application US/08392806A

; Patent No. 5965135

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: New HIV-1 virus isolates of a

; TITLE OF INVENTION: subtype vaccine against HIV-1 virus infections of this subtype

; TITLE OF INVENTION: and method of producing same, use of the HIV-1 virus isolates

; NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price Holman and Stern, PLLC

STREET: 400 Seventh street, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/392,806A

FILING DATE: 20-APR-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/02275

FILING DATE: 25-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 4228787.1

FILING DATE: 29-AUG-1992

Query Match 100.0%; Score 46; DB 4; Length 587;

US-09-646-028-50

Query Match 100.0%; Score 46; DB 4; Length 587;

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 596 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-392-806A-2

Query Match          100.0%; Score 46; DB 2; Length 596;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVNSTQLL 10
Db      137 KPVNSTQLL 146

RESULT 12
US-08-257-490-2

; Sequence 2, Application US/09257490A
; Patent No. 6248328
; GENERAL INFORMATION:
;   APPLICANT: Dietrich, Ursula
;   APPLICANT: Von Briesen, Hagen
;   APPLICANT: Grez, Manuel
;   APPLICANT: Rubsamen-Waigmann, Helga
;   TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its differential
;   TITLE OF INVENTION: diagnostics, a vaccine against HIV-1 virus infections
;   TITLE OF INVENTION: of this subtype and method of producing same, use of
;   FILE REFERENCE: 10496/P585120S1
;   CURRENT APPLICATION NUMBER: US/09/257,490A
;   CURRENT FILING DATE: 1999-02-25
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO: 2
;   LENGTH: 596
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
;   FEATURE: OTHER INFORMATION: HIV-1(D757)

Query Match          100.0%; Score 46; DB 3; Length 596;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVNSTQLL 10
Db      137 KPVNSTQLL 146

RESULT 13
US-08-392-806A-4

; Sequence 4, Application US/08392806A
; Patent No. 5965135
; GENERAL INFORMATION:
;   APPLICANT: New HIV-1 virus isolates of a subtype, vaccine against HIV-1 virus infections of this subtype
;   TITLE OF INVENTION: New HIV-1 virus isolates of a subtype, vaccine against HIV-1 virus infections of this subtype
;   TITLE OF INVENTION: of this subtype, and method of producing same, use of the HIV-1 virus isolates
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Jacobson, Price Holman and Stern, PLPC
;     STREET: 400 Seventh street, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 14
US-09-257-490-4

; Sequence 4, Application US/09257490A
; Patent No. 6248328
; GENERAL INFORMATION:
;   APPLICANT: Dietrich, Ursula
;   APPLICANT: Von Briesen, Hagen
;   APPLICANT: Grez, Manuel
;   APPLICANT: Rubsamen-Waigmann, Helga
;   TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its differential
;   TITLE OF INVENTION: diagnostics, a vaccine against HIV-1 virus infections
;   TITLE OF INVENTION: of this subtype and method of producing same, use of
;   FILE REFERENCE: 10496/P585120S1
;   CURRENT APPLICATION NUMBER: US/09/257,490A
;   CURRENT FILING DATE: 1999-02-25
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO: 4
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
;   FEATURE: OTHER INFORMATION: HIV-1(D747)

Query Match          100.0%; Score 46; DB 3; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVNSTQLL 10
Db      139 KPVNSTQLL 148

RESULT 15
US-09-646-028-52

; Sequence 52, Application US/09646028
; Patent No. 6362347
; GENERAL INFORMATION:
;   APPLICANT: Kwak, Larry
;   APPLICANT: Biragyn, Arya
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
;   TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;   FILE REFERENCE: 14014.0316/p


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CURRENT APPLICATION NUMBER: US/09/646,028  
CURRENT FILING DATE: 2000-09-12;  
PRIOR APPLICATION NUMBER: 60/077,745  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 52  
LENGTH: 601  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/notes=synthetic construct  
US-09-646-028-52

Query Match 100.0%; Score 46; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KPVVSTOLL 10  
||| |||||  
Db 342 KPVVSTOLL 351

Search completed: March 12, 2004, 14:26:19  
Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: March 12, 2004, 14:25:16 ; Search time 34 Seconds  
(without alignments)  
62.104 Million cell updates/sec

Title: PARKIN524.PEP

Perfect score: 46  
Sequence: 1 kpvtql11 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 2115259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Published Applications AA:\*

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2: /cggn2\_6/prodata/2/pbpaa/PCT1\_NEW\_PUB.pep:\*

3: /cggn2\_6/prodata/2/pbpaa/US06\_PUBCOMB.pep:\*

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6: /cggn2\_6/prodata/2/pbpaa/PCTUS\_PUBCOMB.pep:\*

7: /cggn2\_6/prodata/2/pbpaa/US08\_PUBCOMB.pep:\*

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18: /cggn2\_6/prodata/2/pbpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	46	100.0	10 14 US-10-200-708-211	Sequence 211, App
2	46	100.0	10 14 US-10-200-708-328	Sequence 328, App
3	46	100.0	10 14 US-10-200-708-530	Sequence 530, App
4	46	100.0	236 10 US-09-827-688-2	Sequence 53, Appl
5	46	100.0	587 14 US-10-335-394-50	Sequence 50, Appl
6	46	100.0	595 14 US-10-335-394-56	Sequence 56, Appl
7	46	100.0	601 14 US-10-335-394-52	Sequence 52, Appl
8	46	100.0	803 14 US-10-190-435-134	Sequence 134, App
9	46	100.0	803 14 US-10-190-435-135	Sequence 135, App
10	46	100.0	845 14 US-10-190-435-129	Sequence 129, App
11	46	100.0	845 14 US-10-190-435-130	Sequence 130, App
12	46	100.0	845 14 US-10-190-435-143	Sequence 143, App
13	46	100.0	849 14 US-10-190-435-148	Sequence 148, App
14	46	100.0	851 14 US-10-190-435-131	Sequence 131, App
15	100.0	- 851	14 US-10-190-435-149	Sequence 149, App

RESULT 1  
US-10-200-708-211  
; Sequence 211, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DEGROOT, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIORITY APPLICATION NUMBER: US/09/351,036  
; PRIORITY FILING DATE: 1999-07-09  
; PRIORITY APPLICATION NUMBER: 60/092,346  
; PRIORITY FILING DATE: 1998-07-10  
; PRIORITY APPLICATION NUMBER: 60/115,145  
; PRIORITY FILING DATE: 1999-01-08  
; PRIORITY APPLICATION NUMBER: 60/130,677  
; PRIORITY FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 211  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
; US-10-200-708-211  
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Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;  
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Qry 1 KPVTQL11 10  
Db 1 KPVTQL11 10  
RESULT 2  
US-10-200-708-328  
; Sequence 328, Application US/10200708

PUBLICATION NO. US2003180314A1  
GENERAL INFORMATION:

APPLICANT: DEGROOT, Anne S.

TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES

FILE REFERENCE: 17999-001

CURRENT APPLICATION NUMBER: US/10/200,708

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US/99/351,036

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 60/092,346

PRIOR FILING DATE: 1998-07-10

PRIOR APPLICATION NUMBER: 60/115,145

PRIOR FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: 60/1130,677

NUMBER OF SEQ ID NOS: 672

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 328

LENGTH: 10

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-10-200-708-328

Query Match 100.0%; Score 46; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 1 KPVVSTQQLL 10

RESULT 3

US-10-200-708-530

Sequence 530, Application US/10200708

Publication No. US20030180314A1

GENERAL INFORMATION:

APPLICANT: DeGroot, Anne S.

TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES

FILE REFERENCE: 17999-001

CURRENT APPLICATION NUMBER: US/10/200,708

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US/09/351,036

PRIOR FILING DATE: 1999-04-23

PRIOR APPLICATION NUMBER: 60/092,346

PRIOR FILING DATE: 1998-07-10

PRIOR APPLICATION NUMBER: 60/115,145

PRIOR FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: 60/130,677

PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 672

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 530

LENGTH: 10

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-10-200-708-530

Query Match 100.0%; Score 46; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 1 KPVVSTQQLL 10

RESULT 4

US-09-027-698-2

Sequence 2, Application US/09827698

GENERAL INFORMATION:

APPLICANT: ORSON, FRANK

APPLICANT: KINSEY, BERNA

APPLICANT: BHOGAL, BALBIR

TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION DR

FILE REFERENCE: P01943051/1000-0014

CURRENT APPLICATION NUMBER: US/09/827,688

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/195,680

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 236

TYPE: PRT

ORGANISM: HIV U#23

US-09-827-688-2

Query Match 100.0%; Score 46; DB 10; Length 236;

Best Local Similarity 100.0%; Pred. No. 0.31; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 46 KPVVSTQQLL 55

RESULT 5

US-10-335-394-50

Sequence 50, Application US/10335394

Publication No. US20030138452A1

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014-0316/P

CURRENT APPLICATION NUMBER: US/10/335,394

CURRENT FILING DATE: 2002-12-31

PRIOR APPLICATION NUMBER: US/09/646,028

PRIOR FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSBQ for Windows Version 3.0

SEQ ID NO 50

LENGTH: 587

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-10-335-394-50

Query Match 100.0%; Score 46; DB 14; Length 587;

Best Local Similarity 100.0%; Pred. No. 0.84; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 328 KPVVSTQQLL 337

RESULT 6

US-10-335-394-56

Sequence 56, Application US/10335394

Publication No. US20030138452A1

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014-0316/P

CURRENT APPLICATION NUMBER: US/10/335,394

CURRENT FILING DATE: 2002-12-31

PRIOR APPLICATION NUMBER: US/09/646,028  
 PRIOR FILING DATE: 2000-09-12  
 PRIOR APPLICATION NUMBER: 60/077,745  
 PRIOR FILING DATE: 1998-03-12  
 NUMBER OF SEQ ID NOS: 57  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 56  
 LENGTH: 595  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
 US-10-335-394-56  
 Query Match Best Local Similarity 100.0%; Score 46; DB 14; Length 595; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KPVNSTQLL 10  
 Db 336 KPVNSTQLL 345

RESULT 7  
 US-10-335-394-52  
 Sequence 52, Application US/10335394  
 Publication No. US20030138452A1  
 GENERAL INFORMATION:  
 APPLICANT: KWAK, Barry  
 APPLICANT: Biragyn, Larry  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
 FILE REFERENCE: 14014\_0316/P  
 CURRENT APPLICATION NUMBER: US/10/335,394  
 CURRENT FILING DATE: 2002-12-31  
 PRIOR APPLICATION NUMBER: US/09/646,028  
 PRIOR FILING DATE: 2000-09-12  
 PRIOR APPLICATION NUMBER: 60/077,745  
 PRIOR FILING DATE: 1998-03-12  
 NUMBER OF SEQ ID NOS: 57  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 52  
 LENGTH: 601  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
 US-10-335-394-52  
 Query Match Best Local Similarity 100.0%; Score 46; DB 14; Length 601; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KPVNSTQLL 10  
 Db 342 KPVNSTQLL 351

RESULT 8  
 US-10-190-435-134  
 Sequence 134, Application US/10190435  
 Publication No. US20030143248A1  
 GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan J.  
 APPLICANT: VAN RENSBURG, Estrelita J.  
 TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
 FILE REFERENCE: P16133.03 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 LENGTH: 845  
 TYPE: PRT

RESULT 9  
 US-10-190-435-135  
 Sequence 135, Application US/10190435  
 Publication No. US20030143248A1  
 GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan J.  
 APPLICANT: VAN RENSBURG, Estrelita J.  
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 FILE REFERENCE: PPI8133.003 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 NUMBER OF SEQ ID NOS: 319  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 129  
 LENGTH: 803  
 TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: TV012c2.1
US-10-190-435-129
Query Match 100.0%; Score 46; DB 14; Length 845;
Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVVSTQLL 10
Db 242 KPVVSTQLL 251
RESULT 11
US-10-190-435-130
; Sequence 130, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PPI8133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 130
; LENGTH: 845
; TYPE: PRT
; FEATURE: ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: TV012c2.1
US-10-190-435-130
Query Match 100.0%; Score 46; DB 14; Length 845;
Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVVSTQLL 10
Db 242 KPVVSTQLL 251
RESULT 12
US-10-190-435-143
; Sequence 143, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PPI8133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 130
; LENGTH: 845
; TYPE: PRT
; FEATURE: ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: 96BW05.02
US-10-190-435-148
Query Match 100.0%; Score 46; DB 14; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.3; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVVSTQLL 10
Db 250 KPVVSTQLL 259
RESULT 14
US-10-190-435-131
; Sequence 131, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PPI8133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 131
; LENGTH: 851
; TYPE: PRT
; FEATURE: ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: TV006c9.1
US-10-190-435-131
Query Match 100.0%; Score 46; DB 14; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.3; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVVSTQLL 10

```

Db ||||||| KPVVSTQLL 256  
RESULT 15  
US-10-190-435-149  
; Sequence 149, Application US10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: FP18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 149  
; LENGTH: 851  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ETH2220  
US-10-190-435-149

Query Match 100.0%; Score 46; DB 14; Length 851;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy ||||||| KPVVSTQLL 10  
Db 249 KPVVSTQLL 258

Search completed: March 12, 2004, 14:30:42  
Job time : 34 secs

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OM protein - protein search, using sw model

Run on:

March 12, 2004, 14:22:50 ; Search time 21 Seconds

(without alignments)

45.805 Million cell updates/sec

Title: PARKIN524.PEP  
 Perfect score: 46  
 Sequence: 1 kpvvstqlll 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : PIR 78;\*

1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

**ALIGNMENTS**

Result No.	Score	Query Match Length	DB ID	Description
1	46	100.0	495	S31493
2	46	100.0	859	T01672
3	43	93.5	219	S25939
4	43	93.5	729	VCLJJKX
5	43	93.5	843	H44001
6	43	93.5	846	VCLJND
7	43	93.5	847	T02448
8	43	93.5	847	S13289
9	43	93.5	851	S33985
10	43	93.5	852	VCLJBR
11	43	93.5	852	T01216
12	43	93.5	853	S55384
13	43	93.5	854	S13288
14	43	93.5	855	VCLJZR
15	43	93.5	856	VCLJH3
16	43	93.5	856	VCLJVL
17	43	93.5	856	VCLJ3W
18	43	93.5	856	A44963
19	43	93.5	859	VCLJMN
20	43	93.5	861	VCLJLV
21	43	93.5	861	VCLJKB
22	43	93.5	868	VCLJH4
23	42	91.3	806	A44218
24	42	91.3	855	VCLJN2
25	41	89.1	854	VCLJSI
26	40	87.0	877	S4197
27	38	82.6	861	VCLJSC
28	38	80.4	863	A55034
29	34	73.9	224	S71749

**RESULT 1**

S31493

env polyprotein - human immunodeficiency virus type 1, HIV-1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 11-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 26-Aug-1999

C;Accession: S31493

R;Clegg, C.S.

Submitted to the EMBL Data Library, December 1992

A;Reference number: S31493

A;Accession: S31493

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-495 <CUE>

A;Cross-references: EMBL:Z19533; NID:960244; PIDN:CAA79593.1; PID:960245

C;Superfamily: type B retrovirus env polyprotein

C;Keywords: polyprotein

Query Match Similarity 100.0%; Score 46; DB 2; Length 495;

Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy No.	1 kpvvstqlll 10	Db No.	233 kpvvstqlll 242
1		1	
2		2	
3		3	
4		4	
5		5	
6		6	
7		7	
8		8	
9		9	
10		10	
11		11	
12		12	
13		13	
14		14	
15		15	
16		16	
17		17	
18		18	
19		19	
20		20	
21		21	
22		22	
23		23	
24		24	
25		25	
26		26	
27		27	
28		28	
29		29	

**RESULT 2**

T01672

env envelope polyprotein precursor - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 21-Jul-2000

C;Accession: T01672

R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell, 46, 63-74, 1986

A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates

A;Reference number: Z14389; MVID:86245056; PMID:2424612

A;Accession: T01672

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-859 <ALI>

A;Cross-references: EMBL:K03456; NID:960228; PIDN:CAA28016.1; PID:960234

C;Superfamily: type B retrovirus env polyprotein

Query Match 100.0%; Score 46; DB 2; Length 859;

Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy No.	1 kpvvstqlll 10	Db No.	257 kpvvstqlll 266
1		1	
2		2	
3		3	
4		4	
5		5	
6		6	
7		7	
8		8	
9		9	
10		10	
11		11	
12		12	
13		13	
14		14	
15		15	
16		16	
17		17	
18		18	
19		19	
20		20	
21		21	
22		22	
23		23	
24		24	
25		25	
26		26	
27		27	
28		28	
29		29	

## RESULT 3

S25939

env protein - human immunodeficiency virus type 1 (fragment)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Accession: S25939 #sequence\_revision 30-Jan-1998 #text\_change 26-Aug-1999

R/Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.

A;Title: Sequence analysis of original HIV-1

A;Reference number: S25937; MUID:9115604; PMID:2000145

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-219 &lt;GUO&gt;

A;Cross-references: EMBL:X5747; NID:960212; PIDN:CAA40693.1; PID:9388536

A;Experimental source: strain JBB

A;Note: the nucleotide sequence was submitted to the BMBL Data Library, March 1991

A;Gene: env

C;Superfamily: type B retrovirus env polyprotein

C;Keywords: coat protein

Query Match Similarity 93.5%; Score 43; DB 2; Length 219; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 209 RPVVSTQQLL 218

RESULT 4

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-9p32)

C;Accession: B42995 #sequence\_revision 31-Dec-1993 #text\_change 01-Mar-1996

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Accession: B42995 #sequence\_revision 31-Dec-1993 #text\_change 01-Mar-1996

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A;Reference number: A42995; MUID:92351552; PMID:1322587

A;Accession: B42995

A;Molecule type: mRNA

A;Residues: 1-229 &lt;SH1&gt;

A;Cross-references: GB:S41266; GB:D01206

C;Genetics: C;Superfamily: env

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A;Reference number: A42995; MUID:92351552; PMID:1322587

A;Accession: B42995

A;Molecule type: mRNA

A;Residues: 1-229 &lt;SH1&gt;

A;Cross-references: GB:S41266; GB:D01206

C;Genetics: C;Superfamily: type B retrovirus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A;Reference number: A42995; MUID:92351552; PMID:1322587

A;Accession: B42995

A;Molecule type: mRNA

A;Residues: 1-229 &lt;SH1&gt;

A;Cross-references: GB:S41266; GB:D01206

C;Genetics: C;Superfamily: env

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated

A;Reference number: A42995; MUID:92351552; PMID:1322587

A;Accession: B42995

A;Molecule type: mRNA

A;Residues: 1-229 &lt;SH1&gt;

A;Cross-references: GB:S41266; GB:D01206

RESULT 6

VCLJND

env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

C;Accession: JQ0065 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyproto

C;Species: human immunodeficiency virus type 1, HIV-1

A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunod

A;Reference number: JQ0065; MUID:90034200; PMID:2806917

A;Accession: JQ0065

A;Molecule type: DNA

A;Residues: 1-846 &lt;SP1&gt;

A;Cross-references: GB:M21323; NID:9328154; PIDN:AAA4073.1; PID:9328162

A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunod

A;Reference number: JQ0065; MUID:90034200; PMID:2806917

A;Accession: JQ0065

A;Molecule type: DNA

A;Residues: 1-846 &lt;SP1&gt;

A;Cross-references: GB:M21323; NID:9328154; PIDN:AAA4073.1; PID:9328162

A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunod

A;Reference number: JQ0065; MUID:90034200; PMID:2806917

A;Accession: JQ0065

A;Molecule type: DNA

A;Residues: 1-846 &lt;SP1&gt;

A;Cross-references: GB:M21323; NID:9328154; PIDN:AAA4073.1; PID:9328162

A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunod

A;Reference number: JQ0065; MUID:90034200; PMID:2806917

A;Accession: JQ0065

A;Molecule type: DNA

A;Residues: 1-846 &lt;SP1&gt;

A;Cross-references: GB:M21323; NID:9328154; PIDN:AAA4073.1; PID:9328162

A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunod

A;Reference number: JQ0065; MUID:90034200; PMID:2806917

A;Accession: JQ0065

A;Molecule type: DNA

A;Residues: 1-846 &lt;SP1&gt;

H44001

env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)

N;Alternate names: coat polyprotein

C;Accession: S25939 #sequence\_revision 31-Dec-1993 #text\_change 09-Sep-1994

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Accession: H44001 #sequence\_revision 31-Dec-1993 #text\_change 09-Sep-1994

R/Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Accession: H44001

A;Molecule type: DNA

A;Residues: 1-843 &lt;LIV&gt;

A;Cross-references: GB:M93258

C;Genetics:

A;Gene: env

C;Superfamily: type B retrovirus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F;19-35/Region: hydrophobic

F;30-48/Product: coat protein gp120 #status predicted &lt;GP1&gt;

F;49-81/Region: hydrophobic

F;673-789/Region: hydrophobic

F;738-755/Domain: transmembrane #status predicted &lt;TMN&gt;

F;87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,434

Query Match Similarity 93.5%; Score 43; DB 1; Length 843; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 248 RPVVSTQQLL 257

RESULT 5

KPVVSTQQLL

Query Match Similarity 93.5%; Score 43; DB 1; Length 846; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQQLL 10

Db 259 RPVVSTQQLL 268



Query Match 93.5%; Score 43; DB 1; Length 855;  
 Best Local Similarity 90.0%; Pred. No. 0.61;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

---

Qy 1 KPVVSTQLL 10  
 Db 253 RPVVSTQLL 262

RESULT 13

S13288 env protein - human immunodeficiency virus type 1  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C;Accession: S13288  
 R;O'rien, W.A.; Koyanagi, Y.; Nanzie, A.; Zhao, J.Q.; Daigne, A.; Idler, K.; Zack, J.A.  
 Nature 348, 69-73, 1990  
 A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
 A;Reference number: S13288; MUID:91043044; PMID:2172833  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-854 <OBR>  
 C;Superfamily: type B retrovirus env polyprotein

Query Match 93.5%; Score 43; DB 2; Length 854;  
 Best Local Similarity 90.0%; Pred. No. 0.61;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10  
 Db 250 RPVVSTQLL 259

RESULT 14

VCLW3 env polyprotein precursor - human immunodeficiency virus Zr-6  
 C;Alternate names: coat polyprotein  
 C;Species: human immunodeficiency virus Zr-6  
 C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
 C;Accession: D26192  
 R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
 A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
 A;Reference number: A26192; MUID:87248097; PMID:3036660  
 A;Accession: D26192  
 A;Molecule type: DNA  
 A;Residues: 1-855 <SR>  
 C;Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; RID:9329403  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type B retrovirus env polyprotein  
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote  
 P;1-30/Domain: signal sequence #status predicted <SIG>  
 P;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
 P;512-856/Product: transmembrane glycoprotein #status predicted <TMM>  
 P;888-136,-41,156-160,186,197,230,234,211,262,276,289,295,301,312,339,356,386,392,397,406,  
 F;611,616,627,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict  
 Query Match 93.5%; Score 43; DB 1; Length 856;  
 Best Local Similarity 90.0%; Pred. No. 0.61;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10  
 Db 252 RPVVSTQLL 261

Search completed: March 12, 2004, 14:25:44  
 Job Time : 22 secs



FT CARBOHYD 236 236  
 FT CARBOHYD 257 257  
 FT CARBOHYD 271 271  
 FT CARBOHYD 284 284  
 FT CARBOHYD 290 290  
 FT CARBOHYD 296 296  
 FT CARBOHYD 326 326  
 FT CARBOHYD 333 333  
 FT CARBOHYD 349 349  
 FT CARBOHYD 355 355  
 FT CARBOHYD 385 385  
 FT CARBOHYD 391 391  
 FT CARBOHYD 395 395  
 FT CARBOHYD 403 403  
 FT SEQUENCE 421 AA; 47493 MW; 25A575719C22967B CRC64;

Query Match Best Local Similarity 100.0%; Score 46; DB 1; Length 421;  
 Matches 10; Conservative 0; Pred. No. 0.052; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVNSTQLL 10  
 Db 247 KPVNSTQLL 256

RESULT 2  
 ENV\_HV1S3 STANDARD; PRT; 852 AA.

ID ENV\_HV1S3 STANDARD; PRT; 852 AA.  
 AC P19549;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (Gp41)].  
 GN Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
 OS Viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TAXID:11690;  
 RN [1] FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE#90317906; PubMed=2370088;  
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
 RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome." J. Virol. 64:4016-4020 (1990).

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DR EMBL; AY552275; AAO17031; 1;  
 DR PDB; 1MEQ; 11-DEC-02;  
 DR HIV; M38427; ENVSS33.  
 DR InterPro; IPR00328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Cat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.  
 FT SIGNAL 1 31 BY SIMILARITY.  
 FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT DISULFID 507 852 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 156 BY SIMILARITY.  
 FT DISULFID 219 248 BY SIMILARITY.  
 FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 331 BY SIMILARITY.  
 FT DISULFID 377 439 BY SIMILARITY.  
 FT DISULFID 384 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 852 AA; 96663 MW; EEBBFBD23C9910D CRC64;

Query Match Best Local Similarity 100.0%; Score 46; DB 1; Length 852;  
 Matches 10; Conservative 0; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVNSTQLL 10  
 Db 253 KPVNSTQLL 262

RESULT 3  
 ENV\_HV1OY STANDARD; PRT; 855 AA.

ID ENV\_HV1OY STANDARD; PRT; 855 AA.  
 AC P20888;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38 Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (Gp41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 RN NCBI\_TAXID:11699;  
 RN [1] FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE#9014854; PubMed=2559749;  
 RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;  
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot." AIDS 3:707-715(1989).  
 CC 1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONSE INDIVIDUAL.

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CC	EMBL; M26727; AAA83397.1; -.	RP	SEQUENCE FROM N.A.
DR	HIV; M6727; ENVSOVI.	RX	MEDLINE:9512297; PubMed=7826699;
DR	InterPro; IPR00328; Env_GP41.	RA	Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.
DR	InterPro; IPR000777; GPP20.	RT	"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB).";
DR	Pfam; PF00516; GP41; 1.	RL	AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
FT	SIGNAL 1 29	CC	CC
FT	CHAIN 30 509	CC	CC
FT	CHAIN 510 855	CC	CC
FT	DISULFID 553 73	CC	CC
FT	DISULFID 118 210	CC	CC
FT	DISULFID 125 201	CC	CC
FT	DISULFID 130 162	CC	CC
FT	DISULFID 223 252	CC	CC
FT	DISULFID 233 244	CC	CC
FT	DISULFID 301 335	CC	CC
FT	DISULFID 381 442	CC	CC
FT	DISULFID 388 415	CC	CC
FT	CARBODYD 87 415	CC	CC
FT	CARBODYD 134 134	CC	CC
FT	CARBODYD 142 142	CC	CC
FT	CARBODYD 145 145	CC	CC
FT	CARBODYD 161 161	CC	CC
FT	CARBODYD 165 165	CC	CC
FT	CARBODYD 192 192	CC	CC
FT	CARBODYD 202 202	CC	CC
FT	CARBODYD 239 239	CC	CC
FT	CARBODYD 246 246	CC	CC
FT	CARBODYD 267 267	CC	CC
FT	CARBODYD 281 281	CC	CC
FT	CARBODYD 294 294	CC	CC
FT	CARBODYD 300 300	CC	CC
FT	CARBODYD 306 306	CC	CC
FT	CARBODYD 336 336	CC	CC
FT	CARBODYD 359 359	CC	CC
FT	CARBODYD 389 389	CC	CC
FT	CARBODYD 395 395	CC	CC
FT	CARBODYD 399 399	CC	CC
FT	CARBODYD 405 405	CC	CC
FT	CARBODYD 458 458	CC	CC
FT	CARBODYD 610 610	CC	CC
FT	CARBODYD 615 615	CC	CC
FT	CARBODYD 624 624	CC	CC
FT	CARBODYD 636 636	CC	CC
FT	CARBODYD 815 815	CC	CC
SQ	SEQUENCE 855 AA; 97476 MW; 9C982A607ADD2DA CRC64;	CC	CC
Query Match	Best Local Similarity 100.0%; Score 46; DB 1; Length 855;	CC	CC
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	CC
Qy	1 KPVUVTQLL 10	CC	CC
Db	257 KPWNQOLL 266	CC	CC
RESULT 4		CC	CC
ENV_HVILW	ENV_HVILW STANDARD; PRT; 856 AA.	CC	CC
ID	070626;	CC	CC
AC	DT 15-JUL-1998 (Rel. 36, Created)	CC	CC
DT	15-JUL-1998 (Rel. 36, Last sequence update)	CC	CC
DT	10-OCT-2003 (Rel. 42, Last annotation update)	CC	CC
DE	Envelope polyprotein GP60 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].	CC	CC
DE	Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).	CC	CC
GN	Env.	CC	CC
OC	Viruses; Retroviridae; Lentivirus.	CC	CC
OS	NCBI_TaxId=82834;	CC	CC
[1]		CC	CC
Query Match	Best Local Similarity 100.0%; Score 46; DB 1; Length 856;	CC	CC
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	CC
SEQUENCE	856 AA; 96938 MW; 0C241332CF7B6687 CRC64;	CC	CC

Qy	1 KPVVSTQLL 10	FT CARBOHYD 357	N-LINKED (GLCNAC. . .)
Db	252 KPVVSTQLL 261	FT CARBOHYD 364	(POTENTIAL) . . .
RESULT 5	ENV_HV1MA	STANDARD; PRT; 859 AA.	N-LINKED (GLCNAC. . .)
ID ENV_HV1MA		PRT; 859 AA.	(POTENTIAL) . . .
AC P04583;			
DT 13-AUG-1987 (Rel. 05, Created)			
15-JUL-1999 (Rel. 38, Last sequence update)			
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
ENV.			
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).			
OX Retroviruses; Retroviridae; Lentivirus.			
RN [1] NCBI_TaxID=11697;			
RP SEQUENCE FROM N.A.			
RX MEDLINE=86245056; PubMed=2424612;			
RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;			
CC "Generic variability of the AIDS virus; nucleotide sequence analysis of two isolates from African patients.", Cell 46:63-74(1986).			
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EMBL; X04415; CA028016 1; .			
DR T01161; CA00623.1; .			
PIR; T01672; T01672.			
HIV; K03456; ENVMA.			
InterPro; IPR000328; Env GP41.			
DR InterPro; IPR000777; GPI20.			
PFAM; PF00516; GP120; 1.			
DR Pfam; PR00517; GP41; 1.			
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; SIGNAL.			
FT 1 30			
CHAIN 31 513 EXTERIOR MEMBRANE GLYCOPROTEIN.			
DISULFID 514 859 TRANSMEMBRANE GLYCOPROTEIN.			
DISULFID 53 73 BY SIMILARITY.			
DISULFID 118 210 BY SIMILARITY.			
DISULFID 125 201 BY SIMILARITY.			
DISULFID 130 162 BY SIMILARITY.			
DISULFID 223 252 BY SIMILARITY.			
DISULFID 233 244 BY SIMILARITY.			
DISULFID 301 334 BY SIMILARITY.			
DISULFID 380 445 BY SIMILARITY.			
DISULFID 418 418 BY SIMILARITY.			
DISULFID 87 87 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 129 129 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 134 134 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 139 139 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 146 146 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 161 161 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 193 193 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 202 202 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 239 239 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 246 246 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 267 267 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 281 281 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 294 294 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 300 300 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 306 306 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 337 337 N-LINKED (GLCNAC. . .)	(POTENTIAL).		
DISULFID 388 457			
-----			
Qy	1 KPVVSTQLL 10	FT CARBOHYD 357	N-LINKED (GLCNAC. . .)
Db	252 KPVVSTQLL 261	FT CARBOHYD 364	(POTENTIAL) . . .
RESULT 6	ENV_HV1J3	STANDARD; PRT; 867 AA.	N-LINKED (GLCNAC. . .)
ID ENV_HV1J3		PRT; 867 AA.	(POTENTIAL) . . .
AC P12489;			
DT 01-OCT-1989 (Rel. 12, Created)			
15-JUL-1999 (Rel. 38, Last sequence update)			
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
ENV.			
OS Human immunodeficiency virus type 1 (WU isolate) (HIV-1).			
OX Viruses; Retrovirus; Retroviridae; Lentivirus.			
RN [1] NCBI_TaxID=11694;			
RP SEQUENCE FROM N.A.			
RX MEDLINE=89352108; PubMed=2663897;			
RA Komijima N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;			
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of HIV-1 and their expression in bacteria." AIDS Res. Hum. Retroviruses 5:411-419 (1989).			
RL AIDS Res. Hum. Retroviruses 5:411-419 (1989).			
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-----			
EMBL; M21138; AAB03526.1; .			
DR HIV; M21138; ENVSH3.			
DR InterPro; IPR000328; Env GP41.			
DR InterPro; IPR000777; GPI20.			
DR Pfam; PR00516; GP120; 1.			
DR Pfam; PR00517; GP41; 1.			
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT 1 30			
CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.			
DISULFID 517 867 TRANSMEMBRANE GLYCOPROTEIN.			
DISULFID 53 73 BY SIMILARITY.			
DISULFID 118 217 BY SIMILARITY.			
DISULFID 125 208 BY SIMILARITY.			
DISULFID 130 160 BY SIMILARITY.			
DISULFID 230 259 BY SIMILARITY.			
DISULFID 240 251 BY SIMILARITY.			
DISULFID 308 342 BY SIMILARITY.			
DISULFID 388 457 BY SIMILARITY.			

FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 423 423 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 636 636 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 648 648 N-LINKED (GLCNAC. .) (POTENTIAL).

FT SEQUENCE 867 AA; 98399 MW; 5F30146B8E8A0 CRC64;

Query Match 100.0%; Score 46; DB 1; Length 867;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10

Db 264 KPVVSTQLL 273

RESULT 7 ENV\_HV1Z3 STANDARD; PRT; 460 AA.

ID ENV\_HV1Z3 STANDARD; PRT; 460 AA.

AC P12491; 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120)].

GN ENV.

OS Human immunodeficiency virus type 1 (Zaire 3 isolate) (HIV-1).

OC Viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxId:1680; 11] SEQUENCE FROM N.A.

RP MEDLINE=88225978; PubMed=3014529;

RA Willey, R.W., Rutledge, R.A., Folks, T., Theodore, T., Buckner, C.E., Martin, M.A.; "Identification of conserved and divergent domains within the envelope gene of the acquired immunodeficiency syndrome retrovirus."; Proc. Natl. Acad. Sci. U.S.A. 83:5038-5042 (1986).

RT 1- MISCELLANEOUS: THOUGH THIS SEQUENCE CONTAINS A COMPLETE ENV CODING REGION, INSERTION OF AN EXTRA NUCLEOTIDE CREATES A STOP CODON PRIOR TO THE NORMAL TERMINATION, THE AUTHORS SUGGEST THAT THIS VARIATION CAN ACCOUNT FOR THE LACK OF INFECTIVITY OF THIS CLONE.

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CC or send an email to license@isb-sib.ch).

CC CC -----

CC EMBL; K03347; AAA43372.1; -;

CC DR; HIV; K03347; ENVS23; Inter-Pro; IPR00777; GP120.

CC DR Pfam; PF00516; GP120; 1.

CC AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; KW Signal.

CC FT SIGNAL 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.

CC FT CHAIN 30 460 BY SIMILARITY.

CC FT DISUFD 53 73 BY SIMILARITY.

CC FT DISUFD 118 202 BY SIMILARITY.

CC FT DISUFD 125 193 BY SIMILARITY.

CC FT DISUFD 130 149 BY SIMILARITY.

CC FT DISUFD 215 244 BY SIMILARITY.

CC FT DISUFD 225 236 BY SIMILARITY.

CC FT DISUFD 293 326 BY SIMILARITY.

CC FT DISUFD 372 439 BY SIMILARITY.

CC FT DISUFD 379 412 BY SIMILARITY.

CC FT DISUFD 397 404 BY SIMILARITY.

CC FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 180 180 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 285 286 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 327 327 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 380 380 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).

CC FT SEQUENCE 460 AA; 51297 MW; 27B97EB5C7FP50 CRC64;

Query Match 93.5%; Score 43; DB 1; Length 460;

Best Local Similarity 90.0%; Pred. No. 0.24; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 90%; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10

Db 249 KPVVSTQLL 258

RESULT 8 ENV\_HV1Y2 STANDARD; PRT; 843 AA.

ID ENV\_HV1Y2 STANDARD; PRT; 843 AA.

AC P35951; 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (YU-2 isolate) (HTV-1).

OC Viruses; Retrovirdae; Lentivirus.

OX NCBI\_TaxId=36377;

RN [1] SEQUENCE FROM N.A.

CC MEDLINE=9302187; PubMed=1404605;

RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H., Shaw G.M.;

RA -----





FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 202 BY SIMILARITY.  
 FT DISULFID 125 193 BY SIMILARITY.  
 FT DISULFID 130 152 BY SIMILARITY.  
 FT DISULFID 215 244 BY SIMILARITY.  
 FT DISULFID 225 236 BY SIMILARITY.  
 FT DISULFID 372 435 BY SIMILARITY.  
 FT DISULFID 379 408 BY SIMILARITY.  
 FT CARBOHYD 134 134 BY SIMILARITY.  
 FT CARBOHYD 140 140 BY SIMILARITY.  
 FT CARBOHYD 151 151 BY SIMILARITY.  
 FT CARBOHYD 155 155 BY SIMILARITY.  
 FT CARBOHYD 183 183 BY SIMILARITY.  
 FT CARBOHYD 184 184 BY SIMILARITY.  
 FT CARBOHYD 194 194 BY SIMILARITY.  
 FT CARBOHYD 231 231 BY SIMILARITY.  
 FT CARBOHYD 238 238 BY SIMILARITY.  
 FT CARBOHYD 259 259 BY SIMILARITY.  
 FT CARBOHYD 273 273 BY SIMILARITY.  
 FT CARBOHYD 286 286 BY SIMILARITY.  
 FT CARBOHYD 292 292 BY SIMILARITY.  
 FT CARBOHYD 327 327 BY SIMILARITY.  
 FT CARBOHYD 334 334 BY SIMILARITY.  
 FT CARBOHYD 350 350 BY SIMILARITY.  
 FT CARBOHYD 356 356 BY SIMILARITY.  
 FT CARBOHYD 380 380 BY SIMILARITY.  
 FT CARBOHYD 386 386 BY SIMILARITY.  
 FT CARBOHYD 390 390 BY SIMILARITY.  
 FT CARBOHYD 400 400 BY SIMILARITY.  
 FT CARBOHYD 438 438 BY SIMILARITY.  
 FT CARBOHYD 450 450 BY SIMILARITY.  
 FT CARBOHYD 602 602 BY SIMILARITY.  
 FT CARBOHYD 607 607 BY SIMILARITY.  
 FT CARBOHYD 616 616 BY SIMILARITY.  
 FT CARBOHYD 628 628 BY SIMILARITY.  
 SQ SEQUENCE 847 AA; 96466 MW; C0LE33D73A5BCAE CRC64;

Query Match 93.5%; Score 43; DB 1; Length 847;  
 Best Local Similarity 90.0%; Pred. No. 0.43; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVNSTQLL 10  
 Db 249 RPPVSTQQLL 258

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RESULT 12

ENV\_HV1JR STANDARD; PRT; 848 AA.

ID ENV\_HV1JR 24871;  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-2003 (Rel. 42, Last annotation update)

DE Envelope polyprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GPI20); Transmembrane glycoprotein (GP41)].  
 DE ENV.

OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 OC NCBI\_TAXID=11688;  
 RN [1]

RP SOURCE FROM N.A.  
 RA Koyanagi S., Chen I.S.Y.;  
 RL Submitted (DBC-1988) to the HIV data bank.

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CC DISULFID

CC BY SIMILARITY.

CC BY SIMILARITY.

CC BY SIMILARITY.

CC BY SIMILARITY.

CC

CC EXTERIOR MEMBRANE GLYCOPROTEIN.

CC TRANSMEMBRANE GLYCOPROTEIN.

CC BY SIMILARITY.

CC BY SIMILARITY.

CC BY SIMILARITY.

CC

CC BY SIMILARITY.

CC



FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 852 AA; 97203 MW; 2BBB66345DEC15F CRC64;

Query Match 93.5%; Score 43; DB 1; length 852;  
 Best Local Similarity 90.0%; Pred. No. 0.44; 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10  
 Db 252 RPVVSQQLL 261

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RESULT 15

ENV\_HVIEL STANDARD: PRT; 853 AA.

AC P04581; ENV\_HVIEL  
 ID ENV\_HVIEL  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope polyprotein GP60 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE ENV.

OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).

OC Virtues; Retroviridae; Lentivirus.

OX NCBI\_TAXID=11689;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE:86245056; PubMed=2424612;

RA Allizon M., Wain-Hobson S., Montagnier L., Sonigo P.; RT "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients." Cell 46:63-74(1986).

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CC EMBL; K03454; AAA44329; 1; -. DR EMBL; A07108; CA000616; 1; -. DR HIV; K03454; ENVSBLI; -. DR InterPro; IPR000777; GP120. DR InterPro; IPR00322; Env GP41. DR InterPro; IPR000777; GP120. DR PRAM; PR00516; GP120; 1. DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; KW Signal. 1

FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 154 BY SIMILARITY.  
 FT DISULFID 219 248 BY SIMILARITY.  
 FT DISULFID 229 240 BY SIMILARITY.  
 FT DISULFID 297 330 BY SIMILARITY.  
 FT DISULFID 376 442 BY SIMILARITY.  
 FT DISULFID 383 415 BY SIMILARITY.  
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 853 AA; 96721 MW; F9CDB861DA0D07A5 CRC64;

Query Match 93.5%; Score 43; DB 1; length 853;  
 Best Local Similarity 90.0%; Pred. No. 0.44; 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10  
 Db 253 RPVVSQQLL 262

Search completed: March 12, 2004, 14:24:18  
 Job time : 12 secs

GenCore version 5.1.6  
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## Om protein - protein search, using sw model

Run on: March 12, 2004, 14:22:50 ; Search time 40 Seconds

(without alignments)  
78.880 Million cell updates/sec

## Title: PARKIN524.PEP

Perfect score: 46  
Sequence: 1 KPVVSTQLL 10

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 25;\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

RESULT	1
ID	Q9K19
PRIMINARY;	
PRT;	33 AA.
AC	Q9K19;
DT	01-MAY-2000 (TREMBirel. 13, Created)
DT	01-MAY-2000 (TREMBirel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBirel. 24, Last annotation update)
DB	Envelope glycoprotein (Fragment).
GN	ENV.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentivirus.
OX	NCBI_TAXID=11676;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=22020V3_11;
RX	MEDLINE=99094949; PubMed=998014;
RA	Van Dyke R.B., Korber B.T., Popek E., Macken C., Widmayer S.M.,
RA	Barduguez A., Hansen I.C., Wiznia A., Lurzuraga K., Viscarelio R.R.,
RA	Wolinsky S., the Ariel Core Investigators;
RT	"The Ariel Project: A prospective cohort study of maternal-child
RT	transmission of human immunodeficiency virus type 1 in the era of
RT	maternal antiretroviral therapy." J. Infect. Dis. 179:319-328 (1999).
RL	J. Infect. Dis. 179:319-328 (1999).
DR	EMBL: AF12549; AF13327; 1; -;
DR	GO; GO:0019028; C:viral capsid; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR00777; GPI20.
DR	PF00516; GP120; 1.
KW	AIDS; Coat protein; Glycoprotein.
FT	NON_TER 1
SQ	SEQUENCE 33 AA; 3615 MW; 7E5FB44BA535391 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.016; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLL 10

Db	13 KPVVSTQLL 22
<b>RESULT 2</b>	
Q9J414	PRELIMINARY; PRT; 35 AA.
ID Q9J414	
AC Q9J414;	
DT 01-OCT-2000 (TREMBrel. 15, Created)	
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)	
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)	
DE Truncated envelope glycoprotein (Fragment).	
GN ENV.	
OS Human immunodeficiency virus 1.	
OC Viruses; Retroviridae; Lentivirus.	
OX NCBI_TAXID=11676;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=TB24;	
RX MEDLINE=20091829; PubMed=1103611;	
RA Collins K.R., Mayanja-Kizza H., Sullivan B.A., Quinones-Mateu M.E.,	
RT "Greater diversity of HIV-1 quasispecies in HIV-infected individuals with active tuberculosis";	
RL J. Acquir. Immune Defic. Syndr. 24:408-417(2000).	
EMBL AF20177; AACF1854.1; -;	
DR GO; GO:0019028; C:viral capsid; IEA.	
DR GO; GO:0019031; C:viral envelope; IEA.	
DR InterPro; IPR000777; GP120.	
DR Pfam; PF00516; GP120.1.	
KW AIDS; Coat protein; Envelope protein; Glycoprotein.	
FT NON_TER 1 1	
SEQUENCE 35 AA; 3497 MW; F42400992318A39 CRC64;	
Query Match Best Local Similarity 100.0%; Score 46; DB 15; Length 35; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; SQ 1 KPVVSTQLLL 10	
Db 18 KPVVSTQLLL 27	
<b>RESULT 3</b>	
Q9J4HB	PRELIMINARY; PRT; 74 AA.
ID Q9J4HB	
AC Q9J4HB;	
DT 01-OCT-2000 (TREMBrel. 15, Created)	
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)	
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)	
DE Truncated envelope glycoprotein (Fragment).	
GN ENV.	
OS Human immunodeficiency virus 1.	
OC Viruses; Retroviridae; Lentivirus.	
OX NCBI_TAXID=11676;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=TB24;	
RX MEDLINE=20091829; PubMed=11035611;	
RA Collins K.R., Mayanja-Kizza H., Sullivan B.A., Quinones-Mateu M.E.,	
RT "Greater diversity of HIV-1 quasispecies in HIV-infected individuals with active tuberculosis";	
RL J. Acquir. Immune Defic. Syndr. 24:408-417(2000).	
EMBL AF201793; AACF1860.1; -;	
DR GO; GO:0019028; C:viral capsid; IEA.	
DR GO; GO:0019031; C:viral envelope; IEA.	
DR GO; GO:0005198; F:structural molecule activity; IEA.	
DR InterPro; IPR000777; GP120.	
DR Pfam; PF00516; GP120.1.	
KW AIDS; Coat protein; Envelope protein; Glycoprotein.	
FT NON_TER 1 1	
SEQUENCE 85 AA; 9372 MW; 70F92F1CE393D580 CRC64;	
Query Match Best Local Similarity 100.0%; Score 46; DB 15; Length 85; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; SQ 1 KPVVSTQLLL 10	
Db 7 KPVVSTQLLL 16	
<b>RESULT 5</b>	
Q8J9CB	PRELIMINARY; PRT; 85 AA.
ID Q8J9CB	
AC Q8J9CB;	
DT 01-OCT-2002 (TREMBrel. 22, Created)	
DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)	
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)	
DE Envelope glycoprotein (Fragment).	
GN ENV.	
OS Human immunodeficiency virus 1.	
OC Viruses; Retroviridae; Lentivirus.	
OX NCBI_TAXID=11676;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=TB24;	
RX MEDLINE=20091829; PubMed=11035611;	
RA Toosi Z., Arts E.J.;	
RT "Molecular study of an HIV-1 transmission chain 7 years after submission of events";	
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AF490623; AACM0991.1; -;	
DR GO; GO:0019028; C:viral capsid; IEA.	
DR GO; GO:0019031; C:viral envelope; IEA.	
DR InterPro; IPR000777; GP120.	
DR Pfam; PF00516; GP120.1.	
KW AIDS; Coat protein; Envelope protein; Glycoprotein.	
FT NON_TER 1 1	
SQ SEQUENCE 74 AA; 8011 MW; 5AA00D31924528A CRC44;	

DR GO: GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00777; GP120.  
 RC STRAIN=subtype E;  
 RX PMID=9408306; PubMed=10480629;  
 KW AIDS; Coat protein; Glycoprotein.  
 FT NON\_TER 1  
 SQ SEQUENCE 85 AA; 9232 MW; 6034854CF528A3F5 CRC64;  
 Query Match 100.0%; Score 46; DB 15; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KPVVSTQLL 10  
 Db 7 KPVVSTQLL 16

RESULT 6

Q90UB9 PRELIMINARY; PRT; 95 AA.  
 ID Q90UB9  
 RA Gunthard H.F., Havlir D.V., Fuscus S., Zhang Z.-Q., Eron J.J.,  
 Mellors J., Gulick R., Frost S.D., Leigh Brown A.J., Schleif W.,  
 Valentine F., Jonas L., Meibom A., Ignacio C.C., Isaacs R.,  
 RA Gamarni R., Emami E., Haase J.K., Richman D.D., Wong J.K.;  
 RT "Residual human immunodeficiency virus (HIV) type 1 RNA and DNA in  
 lymph nodes and HIV RNA in genital secretions and in cerebrospinal  
 fluid after suppression of viremia for 2 years.";  
 RT J. Infect. Dis. 183:1318-1327(2001).  
 RL EMBL; AF337312; AAK6233.1;-  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00777; GP120.  
 KW AIDS; Coat protein; Glycoprotein.  
 RN [1]\_TaxID=11676;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21192328; PubMed=11294662;  
 RA Gunthard H.F., Havlir D.V., Fuscus S., Zhang Z.-Q., Eron J.J.,  
 Mellors J., Gulick R., Frost S.D., Leigh Brown A.J., Schleif W.,  
 Valentine F., Jonas L., Meibom A., Ignacio C.C., Isaacs R.,  
 RA Gamarni R., Emami E., Haase J.K., Richman D.D., Wong J.K.;  
 RT "Residual human immunodeficiency virus (HIV) type 1 RNA and DNA in  
 lymph nodes and HIV RNA in genital secretions and in cerebrospinal  
 fluid after suppression of viremia for 2 years.";  
 RT J. Infect. Dis. 183:1318-1327(2001).  
 RL EMBL; AF337312; AAK6233.1;-  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR InterPro; IPR00777; GP120.  
 KW AIDS; Coat protein; Glycoprotein.  
 RN [1]\_TaxID=11676;

RESULT 8

Q9QT80 PRELIMINARY; PRT; 99 AA.  
 ID Q9QT80  
 AC Q9QT80;  
 DT 01-MAY-2000 (TREMBrel. 13, Created)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
 DE Envelope glycoprotein gp120 C2V3 region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviroidea; Lentiviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=subtype E;  
 RX MEDLINE=99408506; PubMed=10480629;  
 RA Kato K., Shimo T., Kusagawa S., Sato H., Nohtoni K., Shibamura K.,  
 RA Hien N.T., Chi P.K., Lien T.X., Anh M.H., Long H.T.,  
 RA Bunyarakositon G., Fukushima Y., Honda M., Wasi C., Yamazaki S.,  
 RA Nagai Y., Takebe Y.;  
 RT "Genetic similarity of HIV Type 1 subtype E in a recent outbreak among  
 injecting drug users in Northern Vietnam to strains in Guangxi  
 province of Southern China.";  
 RT AIDS Res. Hum. Retroviruses 15:1157-1168(1999).  
 RL EMBL; AB025084; BA83656.1;-  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Glycoprotein.  
 RN [1]\_TaxID=11676;

RESULT 7

Q9QT87 PRELIMINARY; PRT; 99 AA.  
 ID Q9QT87  
 AC Q9QT87;  
 DT 01-MAY-2000 (TREMBrel. 13, Created)  
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
 DE Envelope glycoprotein gp120 C2V3 region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviroidea; Lentiviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;

Query Match 100.0%; Score 46; DB 15; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KPVVSTQLL 10  
 Db 5 KPVVSTQLL 14

RESULT 8

Q9QT80 PRELIMINARY; PRT; 99 AA.  
 ID Q9QT80  
 AC Q9QT80;  
 DT 01-MAY-2000 (TREMBrel. 13, Created)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
 DE Envelope glycoprotein gp120 C2V3 region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviroidea; Lentiviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;

Query Match 100.0%; Score 46; DB 15; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KPVVSTQLL 10  
 Db 3 KPVVSTQLL 12

**RESULT 9**

01506 PRELIMINARY; PRT; 99 AA.

ID 091506 PRELIMINARY; PRT; 99 AA.

AC 091506; "Identificaiton of Thai HIV-1 Variants in Japan (provisional title)."; [2]

RT Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SUBTYPE\_E;

RX MEDLINE=99146664; PubMed=10024059;

RA Leng H.B., Phalla T., Heng M.B., Takebe Y., AIDS Res. Hum. Retroviruses 15:91-94(1999).

RT "HIV type 1 env subtype E in Cambodia.";

RL AIDS Res. Hum. Retroviruses 15:91-94(1999).

DR EMBL; AB013126; BA033687.1; -;

GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

FT GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR00777; GPI20.

DR Pfam; PF00516; GP120.

KW AIDS; Coat protein; Glycoprotein.

ALDS; Coat protein; Glycoprotein.

NON\_TER 1

FT NON\_TER 1

SQ SEQUENCE 99 AA; 10927 MW; 773564329BR2D1DB CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Db 3 KPVVSTQIIL 12

**RESULT 10**

079317 PRELIMINARY; PRT; 99 AA.

ID 079317 PRELIMINARY; PRT; 99 AA.

AC 079317; "Identificaiton of Thai HIV-1 Variants in Japan (provisional title)."; [2]

RT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

NCBI\_TAXID=11676;

RC STRAIN=SUBTYPE\_E;

RX MEDLINE=99146664; PubMed=10024059;

RA Takebe Y., Fujiwara Y., Sato H., Oka S., Pau C.P., Imai M., Ou C.Y., Weniger B.G., Yamazaki S.; "Identificaiton of Thai HIV-1 Variants in Japan (provisional title)."; [2]

RT "The molecular epidemiology of HIV in Asia.";

RL AIDS 0-0-1994).

DR EMBL; L32085; AAC37879.1; -;

GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0005198; C:viral envelope; IEA.

DR InterPro; IPR00777; GPI20.

DR Pfam; PF00516; GP120. 1.

**RESULT 11**

090779 PRELIMINARY; PRT; 99 AA.

ID 090779 PRELIMINARY; PRT; 99 AA.

AC 090779; "Genetic similarity of HIV Type 1 subtype E in a recent outbreak among injecting drug users in Northern Vietnam to strains in Guangxi province of Southern China.";

RT AIDS Res. Hum. Retroviruses 15:1157-1168(1999).

RA Hien N.T., Chi P.K., Lien T.X., Anh M.H., Long H.T., Bunyakasyotin G., Fukushima Y., Honda M., Wasi C., Yamazaki S., Nagai Y., Takebe Y.

RN "Genetic similarity of HIV Type 1 subtype E in a recent outbreak among injecting drug users in Northern Vietnam to strains in Guangxi province of Southern China.";

DR EMBL; AB025085; BA033657.1; -;

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR InterPro; IPK00777; F:structural molecule activity; IEA.

DR Pfam; PF00516; GP120. 1.

KW AIDS; Coat protein; Glycoprotein.

ALDS; Coat protein; Glycoprotein.

NON\_TER 1

FT NON\_TER 1

SQ SEQUENCE 99 AA; 10578 MW; B544B34E46A5A2C3 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Db 3 KPVVSTQIIL 12

**RESULT 12**

091507 PRELIMINARY; PRT; 99 AA.

ID 091507 PRELIMINARY; PRT; 99 AA.

AC 091507; "Identificaiton of Thai HIV-1 Variants in Japan (provisional title)."; [2]

RT Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SUBTYPE\_E;

RX MEDLINE=99146664; PubMed=10024059;

RA Weniger B.G., Takebe Y., Ou C.Y., Yamazaki S.; "Identificaiton of Thai HIV-1 Variants in Japan (provisional title)."; [2]

RT "The molecular epidemiology of HIV in Asia.";

RL AIDS 0-0-1994).

DR EMBL; L32085; AAC37879.1; -;

GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0005198; C:viral envelope; IEA.

DR InterPro; IPR00777; GPI20.

DR Pfam; PF00516; GP120. 1.

KW AIDS; Coat protein; Glycoprotein.

ALDS; Coat protein; Glycoprotein.

NON\_TER 1

FT NON\_TER 1

SQ SEQUENCE 99 AA; 11012 MW; A07B123AE109DF23 CRC64;

Query Match Best Local Similarity 100.0%; Score 46; DB 15; Length 99;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Db 3 KPVVSTQIIL 12

RA Kusagawa S., Sato H., Kato K., Nohomi K., Shiino T., Samrith C.,  
 RA Lang H.B., Phalla T., Heng M.B., Takebe Y.;  
 RT "HIV type 1 env subtype E in Cambodia.";  
 RL AIDS Res. Hum. Retroviruses 15:91-94(1999).  
 DR EMBL; AB01327; BA33681; -;  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Glycoprotein.  
 FT NON\_TER 1  
 FT NON\_TER 99 99 99 AA; 10966 MW; 92C67C25FB0731CO CRC64;  
 SQ SEQUENCE 99 AA; 10966 MW; 92C67C25FB0731CO CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVNSTQLLL 10  
 Db 3 KPVNSTQLLL 12

RESULT 13

ID 091505 PRELIMINARY; PRT; 99 AA.  
 AC 091505;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DR Envelope glycoprotein (Fragment).  
 DR ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=subtype E;  
 RX MEDLINE=99146664; PubMed=10024059;  
 RA Kubagawa S., Sato H., Kato K., Nohomi K., Shiino T., Samrith C.,  
 RA Leng H.B., Phalla T., Heng M.B., Takebe Y.;  
 RT "HIV type 1 env subtype E in Cambodia.";  
 RL AIDS Res. Hum. Retroviruses 15:91-94(1999).  
 DR GO; GO:0013125; BA33686; 1; -;  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA..  
 DR GO; GO:0005198; F:structural molecule activity; IEA..  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Glycoprotein.  
 FT NON\_TER 1  
 FT NON\_TER 99 99 AA; 11007 MW; 3BD7758D878C2357 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVNSTQLLL 10  
 Db 3 KPVNSTQLLL 12

RESULT 14

ID 091502 PRELIMINARY; PRT; 99 AA.  
 AC 091502;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-JUN-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DR Envelope glycoprotein (Fragment).  
 DR ENV.

OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=subtype E;  
 RX MEDLINE=99146664; PubMed=10024059;  
 RA Kusagawa S., Sato H., Kato K., Nohomi K., Shiino T., Samrith C.,  
 RA Lang H.B., Phalla T., Heng M.B., Takebe Y.;  
 RT "HIV type 1 env subtype E in Cambodia.";  
 RL AIDS Res. Hum. Retroviruses 15:91-94(1999).  
 DR EMBL; AB01321; BA33683; 1; -;  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA..  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Glycoprotein.  
 FT NON\_TER 1  
 FT NON\_TER 99 99 AA; 10969 MW; 5050B7576B0731CS CRC64;  
 SQ SEQUENCE 99 AA; 10969 MW; 5050B7576B0731CS CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVNSTQLLL 10  
 Db 3 KPVNSTQLLL 12

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